Sequence Listing

<110> Botstein,David
     Desnoyers,Luc
     Ferrara,Napoleone
     Fong,Sherman
     Gao,Wei-Qiang
     Goddard,Audrey
     Gurney,Austin L.
     Pan,James
     Roy,Margaret Ann
     Stewart,Timothy A.
     Tumas,Daniel
     Watanabe,Colin K.
     Wood,William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic
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cgggatgacc cgccgggacc cgctcgcaaa taaggtggcc ctggtaacgg 150

cctccaccga cgggatcggc ttcgccatcg cccggcgttt ggcccaggac 200

ggggcccatg tggtcgtcag cagccggaag cagcagaatg tggaccaggc 250

ggtggccacg ctgcaggggg aggggctgag cgtgacgggc accgtgtgcc 300

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2

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taagaaggtt aggcgagcca gaggattgtg ctggcatcgt gtctttcctg 800

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Ala Asn Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly
                 35                  40                  45

Phe Ala Ile Ala Arg Arg Leu Ala Gln Asp Gly Ala His Val Val
                 50                  55                  60

Val Ser Ser Arg Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr
                 65                  70                  75
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3

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Leu Gln Gly Glu Gly Leu Ser Val Thr Gly Thr Val Cys His Val
            80                    85                    90

Gly Lys Ala Glu Asp Arg Glu Arg Leu Val Ala Thr Ala Val Lys
            95                   100                   105

Leu His Gly Gly Ile Asp Ile Leu Val Ser Asn Ala Ala Val Asn
           110                   115                   120

Pro Phe Phe Gly Ser Ile Met Asp Val Thr Glu Glu Val Trp Asp
           125                   130                   135

Lys Thr Leu Asp Ile Asn Val Lys Ala Pro Ala Leu Met Thr Lys
           140                   145                   150

Ala Val Val Pro Glu Met Glu Lys Arg Gly Gly Gly Ser Val Val
           155                   160                   165

Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser Pro Gly Phe Ser
           170                   175                   180

Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu Thr Lys Thr
           185                   190                   195

Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn Cys Leu
           200                   205                   210

Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp Met
           215                   220                   225

Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
           230                   235                   240

Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu
           245                   250                   255

Cys Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val
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Gly Gly Gly Thr Pro Ser Arg Leu
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<210> 5
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5

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aagcgactgc aggagctcga gcggaacgtg cagctcatgc ggcagcagca 1150

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gaggacatcg tgcgagtgtc cagccggctg gagcacctgg agaaggagct 1600

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6

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aaaaaaaatc tttgaaggga c 3121

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<212> PRT
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                20   25   30

Gly Trp Gly Gly Leu Arg Leu Leu Asn Gly Leu Pro Pro Gly Ser
                35   40   45

Phe Val Pro Arg Pro His Thr Ala Pro Leu Gly Gly Ala His Ala
                50   55   60

His Val Leu Gly Met Val Pro Pro Ala Cys Leu Pro Gly Asp Glu
                65   70   75

Val Gly Ser Glu Gln Arg Gly Glu Gln Val Thr Asn Gly Arg Glu
                80   85   90

Ala Gly Ala Glu Leu Leu Thr Glu Val Asn Arg Leu Gly Ser Gly
                95   100   105

7

Ser Ser Ala Ala Ser Glu Glu Glu Glu Glu Glu Glu Pro Pro
                110   115   120

Arg Arg Thr Leu His Leu Arg Arg Asn Arg Ile Ser Asn Cys Ser
                125   130   135

Gln Arg Ala Gly Ala Arg Pro Gly Ser Leu Pro Glu Arg Lys Gly
                140   145   150

Pro Glu Leu Cys Leu Glu Glu Leu Asp Ala Ala Ile Pro Gly Ser
                155   160   165

Arg Ala Val Gly Gly Ser Lys Ala Arg Val Gln Ala Arg Gln Val
                170   175   180

Pro Pro Ala Thr Ala Ser Glu Trp Arg Leu Ala Gln Ala Gln Gln
                185   190   195

Lys Ile Arg Glu Leu Ala Ile Asn Ile Arg Met Lys Glu Glu Leu
                200   205   210

Ile Gly Glu Leu Val Arg Thr Gly Lys Ala Ala Gln Ala Leu Asn
                215   220   225

Arg Gln His Ser Gln Arg Ile Arg Glu Leu Glu Gln Glu Ala Glu
                230   235   240

Gln Val Arg Ala Glu Leu Ser Glu Gly Gln Arg Gln Leu Arg Glu
                245   250   255

Leu Glu Gly Lys Glu Leu Gln Asp Ala Gly Glu Arg Ser Arg Leu
                260   265   270

Gln Glu Phe Arg Arg Arg Val Ala Ala Ala Gln Ser Gln Val Gln
                275   280   285

Val Leu Lys Glu Lys Lys Gln Ala Thr Glu Arg Leu Val Ser Leu
                290   295   300

Ser Ala Gln Ser Glu Lys Arg Leu Gln Glu Leu Glu Arg Asn Val
                305   310   315

Gln Leu Met Arg Gln Gln Gln Gly Gln Leu Gln Arg Arg Leu Arg
                320   325   330

Glu Glu Thr Glu Gln Lys Arg Arg Leu Glu Ala Glu Met Ser Lys
                335   340   345

Arg Gln His Arg Val Lys Glu Leu Glu Leu Lys His Glu Gln Gln
                350   355   360

Gln Lys Ile Leu Lys Ile Lys Thr Glu Glu Ile Ala Ala Phe Gln
                365   370   375

Arg Lys Arg Arg Ser Gly Ser Asn Gly Ser Val Val Ser Leu Glu
                380   385   390

Gln Gln Gln Lys Ile Glu Glu Gln Lys Lys Trp Leu Asp Gln Glu

8

Met Glu Lys Val Leu Gln Gln Arg Arg Ala Leu Glu Glu Leu Gly
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Glu Glu Leu His Lys Arg Glu Ala Ile Leu Ala Lys Lys Glu Ala
            425   430   435

Leu Met Gln Glu Lys Thr Gly Leu Glu Ser Lys Arg Leu Arg Ser
            440   445   450

Ser Gln Ala Leu Asn Glu Asp Ile Val Arg Val Ser Ser Arg Leu
            455   460   465

Glu His Leu Glu Lys Glu Leu Ser Glu Lys Ser Gly Gln Leu Arg
            470   475   480

Gln Gly Ser Ala Gln Ser Gln Gln Gln Ile Arg Gly Glu Ile Asp
            485   490   495

Ser Leu Arg Gln Glu Lys Asp Ser Leu Leu Lys Gln Arg Leu Glu
            500   505   510

Ile Asp Gly Lys Leu Arg Gln Gly Ser Leu Leu Ser Pro Glu Glu
            515   520   525

Glu Arg Thr Leu Phe Gln Leu Asp Glu Ala Ile Glu Ala Leu Asp
            530   535   540

Ala Ala Ile Glu Tyr Lys Asn Glu Ala Ile Thr Cys Arg Gln Arg
            545   550   555

Val Leu Arg Ala Ser Ala Ser Leu Leu Ser Gln Cys Glu Met Asn
            560   565   570

Leu Met Ala Lys Leu Ser Tyr Leu Ser Ser Ser Glu Thr Arg Ala
            575   580   585

Leu Leu Cys Lys Tyr Phe Asp Lys Val Val Thr Leu Arg Glu Glu
            590   595   600

Gln His Gln Gln Gln Ile Ala Phe Ser Glu Leu Glu Met Gln Leu
            605   610   615

Glu Glu Gln Gln Arg Leu Val Tyr Trp Leu Glu Val Ala Leu Glu
            620   625   630

Arg Gln Arg Leu Glu Met Asp Arg Gln Leu Thr Leu Gln Gln Lys
            635   640   645

Glu His Glu Gln Asn Met Gln Leu Leu Leu Gln Gln Ser Arg Asp
            650   655   660

His Leu Gly Glu Gly Leu Ala Asp Ser Arg Arg Gln Tyr Glu Ala
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Arg Ile Gln Ala Leu Glu Lys Glu Leu Gly Arg Tyr Met Trp Ile
            680   685   690

9

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Asn Gln Glu Leu Lys Gln Lys Leu Gly Gly Val Asn Ala Val Gly
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His Ser Arg Gly Gly Glu Lys Arg Ser Leu Cys Ser Glu Gly Arg
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Gln Ala Pro Gly Asn Glu Asp Glu Leu His Leu Ala Pro Glu Leu
                725                 730                 735

Leu Trp Leu Ser Pro Leu Thr Glu Gly Ala Pro Arg Thr Arg Glu
                740                 745                 750

Glu Thr Arg Asp Leu Val His Ala Pro Leu Pro Leu Thr Trp Lys
                755                 760                 765

Arg Ser Ser Leu Cys Gly Glu Glu Gln Gly Ser Pro Glu Glu Leu
                770                 775                 780

Arg Gln Arg Glu Ala Ala Glu Pro Leu Val Gly Arg Val Leu Pro
                785                 790                 795

Val Gly Glu Ala Gly Leu Pro Trp Asn Phe Gly Pro Leu Ser Lys
                800                 805                 810
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Arg Lys Asn Pro Leu
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<213> Homo sapiens

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                20                  25                  30

Gly Ser Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn
                35                  40                  45

Lys Ile Tyr Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile
                50                  55                  60

Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe
                65                  70                  75

Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln
                80                  85                  90

Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln
                95                  100                 105

Cys His Leu Ser Pro Ile Ser Arg Ser Cys Thr Arg Asn Arg Arg
                110                 115                 120

His Val Leu Tyr Pro
                125
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<210> 10
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<212> DNA
<213> Homo sapiens

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ggcgccaggg tggccccccgg ggcgcgcttg gtctcggaga agcggggacg 200

aggccggagg atgagcgact gagggcgacg cgggcactga cgcgagttgg 250

ggccgcgact accggcagct gacagcgcga tgagcgactc cccagagacg 300

ccctagcccg gtgtgcgcgc caggcggagc gcgcaggtgg ggctgggctg 350
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11

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cttttgatga ggaataatgg aaaattgttg gtacttttcc ttttcttgat 1700

aacagttact acaacagaag gaaatggata tatttcaaaa catcaacaag 1750

aactttgggc ataaaatcct tctctaaata aatgtgctat tttcacagta 1800
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12

agtacacaaa agtacactat tatatatcaa atgtatttct ataatccctc 1850

cattagagag cttatataag tgttttctat agatgcagat taaaaatgct 1900

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<210> 11
<211> 325
<212> PRT
<213> Homo sapiens

<400> 11
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                20                  25                  30

Ile Pro Leu Glu Lys Leu Ala Gln Ala Pro Glu Gln Pro Gly Gln
                35                  40                  45

Glu Lys Arg Glu His Ala Thr Arg Asp Gly Pro Gly Arg Val Asn
                50                  55                  60

Glu Leu Gly Arg Pro Ala Arg Asp Glu Gly Gly Ser Gly Arg Asp
                65                  70                  75

Trp Lys Ser Lys Ser Gly Arg Gly Leu Ala Gly Arg Glu Pro Trp
                80                  85                  90

Ser Lys Leu Lys Gln Ala Trp Val Ser Gln Gly Gly Gly Ala Lys
                95                  100                 105

Ala Gly Asp Leu Gln Val Arg Pro Arg Gly Asp Thr Pro Gln Ala
                110                 115                 120

Glu Ala Leu Ala Ala Ala Ala Gln Asp Ala Ile Gly Pro Glu Leu
                125                 130                 135

Ala Pro Thr Pro Glu Pro Pro Glu Glu Tyr Val Tyr Pro Asp Tyr
                140                 145                 150

Arg Gly Lys Gly Cys Val Asp Glu Ser Gly Phe Val Tyr Ala Ile
                155                 160                 165

Gly Glu Lys Phe Ala Pro Gly Pro Ser Ala Cys Pro Cys Leu Cys
                170                 175                 180

Thr Glu Glu Gly Pro Leu Cys Ala Gln Pro Glu Cys Pro Arg Leu
                185                 190                 195

His Pro Arg Cys Ile His Val Asp Thr Ser Gln Cys Cys Pro Gln
                200                 205                 210

Cys Lys Glu Arg Lys Asn Tyr Cys Glu Phe Arg Gly Lys Thr Tyr
                215                 220                 225

Gln Thr Leu Glu Glu Phe Val Val Ser Pro Cys Glu Arg Cys Arg
```

13

```
                        230               235               240

    Cys Glu Ala Asn Gly Glu Val Leu Cys Thr Val Ser Ala Cys Pro
                    245               250               255

    Gln Thr Glu Cys Val Asp Pro Val Tyr Glu Pro Asp Gln Cys Cys
                    260               265               270

    Pro Ile Cys Lys Asn Gly Pro Asn Cys Phe Ala Glu Thr Ala Val
                    275               280               285

    Ile Pro Ala Gly Arg Glu Val Lys Thr Asp Glu Cys Thr Ile Cys
                    290               295               300

    His Cys Thr Tyr Glu Glu Gly Thr Trp Arg Ile Glu Arg Gln Ala
                    305               310               315

    Met Cys Thr Arg His Glu Cys Arg Gln Met
                    320               325
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<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 12
 gaggtgtcgc tgtgaagcca acgg 24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 13
 cgctcgattc tccatgtgcc ttcc 24

<210> 14
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 14
 gacggagtgt gtggaccctg tgtacgagcc tgatcagtgc tgtcc 45

<210> 15
<211> 1587
<212> DNA
<213> Homo sapiens

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tcatcctccc actgccagga gtgcaggcgc tgctctgcca gtttgggaca 100

gttcagcatg tgtggaaggt gtccgaccta ccccggcaat ggacccctaa 150

gaacaccagc tgcgacagcg gcttggggtg ccaggacacg ttgatgctca 200

ttgagagcgg accccaagtg agcctggtgc tctccaaggg ctgcacggag 250

gccaaggacc aggagccccg cgtcactgag caccggatgg gccccggcct 300

ctccctgatc tcctacacct tcgtgtgccg ccaggaggac ttctgcaaca 350

acctcgttaa ctccctcccg ctttgggccc cacagccccc agcagaccca 400

ggatccttga ggtgcccagt ctgcttgtct atggaaggct gtctggaggg 450

gacaacagaa gagatctgcc ccaaggggac cacacactgt tatgatggcc 500

tcctcaggct caggggagga ggcatcttct ccaatctgag agtccaggga 550

tgcatgcccc agccaggttg caacctgctc aatgggacac aggaaattgg 600

gcccgtgggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650

atcgggggac caccattatg acacacggaa acttggctca agaacccact 700

gattggacca catcgaatac cgagatgtgc gaggtggggc aggtgtgtca 750

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tggtggggag tggtttgccc ttcctgctaa ctctattacc cccacgattc 1350

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aatggccttg gacaccagat tctttcccat tctgtccatg aatcatcttc 1450
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15

```
     cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500

     gcctggagca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550

     gctgcatgta tctgataata cagaccctgt cctttca 1587
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<210> 16
<211> 437
<212> PRT
<213> Homo sapiens

<400> 16
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 Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro
  1               5                  10                  15

 Leu Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln
                 20                  25                  30

 His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys
                 35                  40                  45

 Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met
                 50                  55                  60

 Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly
                 65                  70                  75

 Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
                 80                  85                  90

 Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
                 95                 100                 105

 Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
                110                 115                 120

 Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
                125                 130                 135

 Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
                140                 145                 150

 Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu
                155                 160                 165

 Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met
                170                 175                 180

 Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly
                185                 190                 195

 Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr
                200                 205                 210

 Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln
                215                 220                 225

 Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val
```

16

```
                        230                      235                      240

      Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu
                        245                      250                      255

      Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala
                        260                      265                      270

      Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val
                        275                      280                      285

      Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn
                        290                      295                      300

      Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln
                        305                      310                      315

      Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln
                        320                      325                      330

      Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro
                        335                      340                      345

      Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly
                        350                      355                      360

      Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln
                        365                      370                      375

      Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe
                        380                      385                      390

      Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His
                        395                      400                      405

      Glu Gly Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val
                        410                      415                      420

      Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro
                        425                      430                      435

      Ser Cys
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<210> 17
<211> 2387
<212> DNA
<213> Homo sapiens

<400> 17
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cgacgatgct acgcgcgccc ggctgcctcc tccggacctc cgtagcgcct 50

gccgcggccc tggctgcggc gctgctctcg tcgcttgcgc gctgctctct 100

tctagagccg agggacccgg tggcctcgtc gctcagcccc tatttcggca 150

ccaagactcg ctacgaggat gtcaacccccg tgctattgtc gggccccgag 200
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17

gctccgtggc gggaccctga gctgctggag gggacctgca ccccggtgca 250

gctggtcgcc ctcattcgcc acggcacccg ctaccccacg gtcaaacaga 300

tccgcaagct gaggcagctg cacgggttgc tgcaggcccg cgggtccagg 350

gatggcgggg ctagtagtac cggcagccgc gacctgggtg cagcgctggc 400

cgactggcct ttgtggtacg cggactggat ggacgggcag ctagtagaga 450

agggacggca ggatatgcga cagctggcgc tgcgtctggc ctcgctcttc 500

ccggcccttt tcagccgtga gaactacggc cgcctgcggc tcatcaccag 550

ttccaagcac cgctgcatgg atagcagcgc cgccttcctg caggggctgt 600

ggcagcacta ccaccctggc ttgccgccgc cggacgtcgc agatatggag 650

tttggacctc aacagttaa tgataaacta atgagatttt ttgatcactg 700

tgagaagttt ttaactgaag tagaaaaaaa tgctacagct ctttatcacg 750

tggaagcctt caaaactgga ccagaaatgc agaacatttt aaaaaaagtt 800

gcagctactt tgcaagtgcc agtaaatgat ttaaatgcag atttaattca 850

agtagccttt ttcacctgtt catttgacct ggcaattaaa ggtgttaaat 900

ctccttggtg tgatgttttt gacatagatg atgcaaaggt attagaatat 950

ttaaatgatc tgaaacaata ttggaaaaga ggatatgggt atactattaa 1000

cagtcgatcc agctgcacct tgtttcagga tatctttcag cacttggaca 1050

aagcagttga acagaaacaa aggtctcagc caatttcttc tccagtcatc 1100

ctccagtttg gtcatgcaga gactcttctt ccactgcttt ctctcatggg 1150

ctacttcaaa gacaaggaac ccctaacagc gtacaattac aaaaaacaaa 1200

tgcatcggaa gttccgaagt ggtctcattg taccttatgc ctcgaacctg 1250

atatttgtgc tttaccactg tgaaaatgct aagactccta agaacaatt 1300

ccgagtgcag atgttattaa atgaaaaggt gttacctttg gcttactcac 1350

aagaaactgt ttcattttat gaagatctga gaaccacta caaggacatc 1400

cttcagagtt gtcaaaccag tgaagaatgt gaattagcaa gggctaacag 1450

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acaggaagct tttatattac ttgagtattt ctgtctttc acagaaaaac 1600

attgggtttc tctctgggtt tggacatgaa atgtaagaaa agattttttca 1650

18

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ctggagcagc tctcttaagg agaaacaaat ctatttagag aaacagctgg 1700

ccctgcaaat gtttacagaa atgaaattct tcctacttat ataagaaatc 1750

tcacactgag atagaattgt gatttcataa taacacttga aaagtgctgg 1800

agtaacaaaa tatctcagtt ggaccatcct taacttgatt gaactgtcta 1850

ggaactttac agattgttct gcagttctct cttcttttcc tcaggtagga 1900

cagctctagc attttcttaa tcaggaatat tgtggtaagc tgggagtatc 1950

actctggaag aaagtaacat ctccagatga gaatttgaaa caagaaacag 2000

agtgttgtaa aaggacacct tcactgaagc aagtcggaaa gtacaatgaa 2050

aataaatatt tttggtattt atttatgaaa tatttgaaca ttttttcaat 2100

aattcctttt tacttctagg aagtctcaaa agaccatctt aaattattat 2150

atgtttggac aattagcaac aagtcagata gttagaatcg aagtttttca 2200

aatccattgc ttagctaact ttttcattct gtcacttggc ttcgattttt 2250

atattttcct attatatgaa atgtatcttt tggttgtttg atttttcttt 2300

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ctataataaa gaaaattctt gtgactttaa aaaaaaa 2387
```

<210> 18
<211> 487
<212> PRT
<213> Homo sapiens

<400> 18

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Met Leu Arg Ala Pro Gly Cys Leu Leu Arg Thr Ser Val Ala Pro
 1               5                  10                  15

Ala Ala Ala Leu Ala Ala Ala Leu Leu Ser Ser Leu Ala Arg Cys
                20                  25                  30

Ser Leu Leu Glu Pro Arg Asp Pro Val Ala Ser Ser Leu Ser Pro
                35                  40                  45

Tyr Phe Gly Thr Lys Thr Arg Tyr Glu Asp Val Asn Pro Val Leu
                50                  55                  60

Leu Ser Gly Pro Glu Ala Pro Trp Arg Asp Pro Glu Leu Leu Glu
                65                  70                  75

Gly Thr Cys Thr Pro Val Gln Leu Val Ala Leu Ile Arg His Gly
                80                  85                  90

Thr Arg Tyr Pro Thr Val Lys Gln Ile Arg Lys Leu Arg Gln Leu
                95                  100                 105

His Gly Leu Leu Gln Ala Arg Gly Ser Arg Asp Gly Gly Ala Ser
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19

Ser Thr Gly Ser Arg Asp Leu Gly Ala Ala Leu Ala Asp Trp Pro
            125   130   135

Leu Trp Tyr Ala Asp Trp Met Asp Gly Gln Leu Val Glu Lys Gly
            140   145   150

Arg Gln Asp Met Arg Gln Leu Ala Leu Arg Leu Ala Ser Leu Phe
            155   160   165

Pro Ala Leu Phe Ser Arg Glu Asn Tyr Gly Arg Leu Arg Leu Ile
            170   175   180

Thr Ser Ser Lys His Arg Cys Met Asp Ser Ser Ala Ala Phe Leu
            185   190   195

Gln Gly Leu Trp Gln His Tyr His Pro Gly Leu Pro Pro Pro Asp
            200   205   210

Val Ala Asp Met Glu Phe Gly Pro Pro Thr Val Asn Asp Lys Leu
            215   220   225

Met Arg Phe Phe Asp His Cys Glu Lys Phe Leu Thr Glu Val Glu
            230   235   240

Lys Asn Ala Thr Ala Leu Tyr His Val Glu Ala Phe Lys Thr Gly
            245   250   255

Pro Glu Met Gln Asn Ile Leu Lys Lys Val Ala Ala Thr Leu Gln
            260   265   270

Val Pro Val Asn Asp Leu Asn Ala Asp Leu Ile Gln Val Ala Phe
            275   280   285

Phe Thr Cys Ser Phe Asp Leu Ala Ile Lys Gly Val Lys Ser Pro
            290   295   300

Trp Cys Asp Val Phe Asp Ile Asp Asp Ala Lys Val Leu Glu Tyr
            305   310   315

Leu Asn Asp Leu Lys Gln Tyr Trp Lys Arg Gly Tyr Gly Tyr Thr
            320   325   330

Ile Asn Ser Arg Ser Ser Cys Thr Leu Phe Gln Asp Ile Phe Gln
            335   340   345

His Leu Asp Lys Ala Val Glu Gln Lys Gln Arg Ser Gln Pro Ile
            350   355   360

Ser Ser Pro Val Ile Leu Gln Phe Gly His Ala Glu Thr Leu Leu
            365   370   375

Pro Leu Leu Ser Leu Met Gly Tyr Phe Lys Asp Lys Glu Pro Leu
            380   385   390

Thr Ala Tyr Asn Tyr Lys Lys Gln Met His Arg Lys Phe Arg Ser
            395   400   405

20

```
Gly Leu Ile Val Pro Tyr Ala Ser Asn Leu Ile Phe Val Leu Tyr
              410             415                 420

His Cys Glu Asn Ala Lys Thr Pro Lys Glu Gln Phe Arg Val Gln
              425             430                 435

Met Leu Leu Asn Glu Lys Val Leu Pro Leu Ala Tyr Ser Gln Glu
              440             445                 450

Thr Val Ser Phe Tyr Glu Asp Leu Lys Asn His Tyr Lys Asp Ile
              455             460                 465

Leu Gln Ser Cys Gln Thr Ser Glu Glu Cys Glu Leu Ala Arg Ala
              470             475                 480

Asn Ser Thr Ser Asp Glu Leu
              485
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<210> 19
<211> 3554
<212> DNA
<213> Homo sapiens

<400> 19

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atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100

cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150

tcaaatccag caatcgaacc ccagtggtac aggaatttga aagtgtggaa 200

ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250

gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300

ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350

aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400

cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450

ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500

ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550

ccggcctcac tacagctggt atcgcaatga tgtaccactg cccacggatt 600

ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650

acaggcactt ggtgttcac tgctgttcac aaggacgact ctgggcagta 700

ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800

gttgtccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850
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21

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cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900

acccagggaa accagatgga gttaactaca tccgcactga cgaggagggc 950

gacttcagac acaagtcatc gtttgtgatc tgagacccgc ggtgtggctg 1000

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agcagcgcat cccggcggga acccagaaaa ggcttcttac acagcagcct 1450

tacttcatcg gcccacagac accaccgcag tttcttctta aaggctctgc 1500

tgatcggtgt tgcagtgtcc attgtggaga agctttttgg atcagcattt 1550

tgtaaaaaca accaaaatca ggaaggtaaa ttggttgctg gaagagggat 1600

cttgcctgag gaaccctgct tgtccaacag ggtgtcagga tttaaggaaa 1650

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tattttgatt attgaaaaga aaatttctat ttaaactgta aatatattgt 1800

catacaatgt taaataacct atttttttaa aaaagttcaa cttaaggtag 1850

aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900

ttttacccaa ggaatcctct catggaagtt tactgtgatg ttccttttct 1950

cacacaagtt ttagcctttt tcacaaggga actcatactg tctacacatc 2000

agaccatagt tgcttaggaa acctttaaaa attccagtta agcaatgttg 2050

aaatcagttt gcatctcttc aaaagaaacc tctcaggtta gctttgaact 2100

gcctcttcct gagatgacta ggacagtctg tacccagagg ccacccagaa 2150

gccctcagat gtacatacac agatgccagt cagctcctgg ggttgcgcca 2200

ggcgcccccg ctctagctca ctgttgcctc gctgtctgcc aggaggccct 2250

gccatccttg ggccctggca gtggctgtgt cccagtgagc tttactcacg 2300
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22

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tggcccttgc ttcatccagc acagctctca ggtgggcact gcagggacac 2350

tggtgtcttc catgtagcgt cccagctttg ggctcctgta acagacctct 2400

ttttggttat ggatggctca caaaataggg cccccaatgc tatttttttt 2450

ttttaagttt gtttaattat ttgttaagat tgtctaaggc caaaggcaat 2500

tgcgaaatca agtctgtcaa gtacaataac atttttaaaa gaaaatggat 2550

cccactgttc ctctttgcca cagagaaagc acccagacgc cacaggctct 2600

gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650

aaagaacgtc aggtggagca gccaggtgaa aggcctggcg gggaggaaag 2700

tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750

atccgccgga gacactgctc ccatttgtgg ggggacatta gcaacatcac 2800

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ttggggattc acgctccagc ctccttcttg gttgtcatag tgatagggta 3250

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tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350

gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatttt 3400

aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450

gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500

caccgtaatt tggcatttgt ttaacctcat ttataaaagc ttcaaaaaaa 3550

ccca 3554
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<210> 20
<211> 310
<212> PRT
<213> Homo sapiens

<400> 20

23

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Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu
 1               5                  10               15

Pro Asp Phe Phe Leu Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly
               20                  25               30

Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu
               35                  40               45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
               50                  55               60

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
               65                  70               75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
               80                  85               90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
               95                 100              105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
               110                115              120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
               125                130              135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
               140                145              150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
               155                160              165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
               170                175              180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
               185                190              195

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
               200                205              210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
               215                220              225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
               230                235              240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
               245                250              255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
               260                265              270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
               275                280              285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
```

24

Asp Phe Arg His Lys Ser Ser Phe Val Ile
                    305   310

<210> 21
<211> 3437
<212> DNA
<213> Homo sapiens

<400> 21
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 gagccgacga cagcgagttc caggcgctgc tggacatctg gtttccggag 150

 gagaagccac tgcccaccgc cttcctggtg gacacatcgg aggaggcgct 200

 gctgcttcct gactggctga agctgcgcat gatccgttct gaggtgctcc 250

 gcctggtgga cgccgccctg caggacctgg agccgcagca gctgctgctg 300

 ttcgtgcagt cgtttggcat ccccgtgtcc agcatgagca aactcctcca 350

 gttcctggac caggcagtgg cccacgaccc ccagactctg gagcagaaca 400

 tcatggacaa gaattacatg gcccacctgg tggaggtcca gcatgagcgc 450

 ggcgcctccg gaggccagac tttccactcc ttgctcacag cctccctgcc 500

 gccccgccga gacagcacag aggcacccaa accaaagagc agcccagagc 550

 agcccatagg ccagggccgg attcgggtgg ggacccagct ccgggtgctg 600

 ggccctgagg acgacctggc tggcatgttc ctccagattt tcccgctcag 650

 cccggaccct cggtggcaga gctccagtcc ccgccccgtg gccctcgccc 700

 tgcagcaggc cctgggccag gagctggccc gcgtcgtcca gggcagcccc 750

 gaggtgccgg gcatcacggt gcgtgtcctg caggccctcg ccaccctgct 800

 cagctcccca cacggcggtg ccctggtgat gtccatgcac cgtagccact 850

 tcctggcctg cccgctgctg cgccagctct gccagtacca gcgctgtgtg 900

 ccacaggaca ccggcttctc ctcgctcttc ctgaaggtgc tcctgcagat 950

 gctgcagtgg ctggacagcc ctggcgtgga gggcgggccc ctgcgggcac 1000

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 gtgcgagggg ggctcctgcg cctggccgag gccctggcct tccgtcagga 1100

 cctggaggtg gtcagctcca ccgtccgtgc cgtcatcgcc accctgaggt 1150

 ctggggagca gtgcagcgtg gagccggacc tgatcagcaa agtcctccag 1200

25

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gggaagccgg gtgcggacgg tggcagcctg gaggccgtgc ggctggggcc 1400

ctcgtcaggc ctcctagtgg actggctgga aatgctggac cccgaggtgg 1450

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acctgcccat gatcgcggcg ctcctgcacg gccgcaccca cctcaacttc 2250

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agcacgccga cccgctccac gacctgtcct tcgacaacag tgacctggtg 2550

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gaccgaccga ggcctggacg aagagggcga ggaggagagc tcagccggct 2650
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26

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cettgcccct ggtcagcgtc tccctgttca cccctctgac cgcggccgag 2700

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<210> 22
<211> 1029
<212> PRT
<213> Homo sapiens

<400> 22
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 Gly Pro Pro Arg Ala Asp Asp Ser Glu Phe Gln Ala Leu Leu Asp
                 20                  25                  30

 Ile Trp Phe Pro Glu Glu Lys Pro Leu Pro Thr Ala Phe Leu Val
                 35                  40                  45

 Asp Thr Ser Glu Glu Ala Leu Leu Leu Pro Asp Trp Leu Lys Leu
                 50                  55                  60

 Arg Met Ile Arg Ser Glu Val Leu Arg Leu Val Asp Ala Ala Leu
                 65                  70                  75

 Gln Asp Leu Glu Pro Gln Gln Leu Leu Leu Phe Val Gln Ser Phe
                 80                  85                  90

 Gly Ile Pro Val Ser Ser Met Ser Lys Leu Leu Gln Phe Leu Asp
                 95                 100                 105
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27

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Gln Ala Val Ala His Asp Pro Gln Thr Leu Glu Gln Asn Ile Met
                110                 115                 120

Asp Lys Asn Tyr Met Ala His Leu Val Glu Val Gln His Glu Arg
                125                 130                 135

Gly Ala Ser Gly Gly Gln Thr Phe His Ser Leu Leu Thr Ala Ser
                140                 145                 150

Leu Pro Pro Arg Arg Asp Ser Thr Glu Ala Pro Lys Pro Lys Ser
                155                 160                 165

Ser Pro Glu Gln Pro Ile Gly Gln Gly Arg Ile Arg Val Gly Thr
                170                 175                 180

Gln Leu Arg Val Leu Gly Pro Glu Asp Asp Leu Ala Gly Met Phe
                185                 190                 195

Leu Gln Ile Phe Pro Leu Ser Pro Asp Pro Arg Trp Gln Ser Ser
                200                 205                 210

Ser Pro Arg Pro Val Ala Leu Ala Leu Gln Gln Ala Leu Gly Gln
                215                 220                 225

Glu Leu Ala Arg Val Val Gln Gly Ser Pro Glu Val Pro Gly Ile
                230                 235                 240

Thr Val Arg Val Leu Gln Ala Leu Ala Thr Leu Leu Ser Ser Pro
                245                 250                 255

His Gly Gly Ala Leu Val Met Ser Met His Arg Ser His Phe Leu
                260                 265                 270

Ala Cys Pro Leu Leu Arg Gln Leu Cys Gln Tyr Gln Arg Cys Val
                275                 280                 285

Pro Gln Asp Thr Gly Phe Ser Ser Leu Phe Leu Lys Val Leu Leu
                290                 295                 300

Gln Met Leu Gln Trp Leu Asp Ser Pro Gly Val Glu Gly Gly Pro
                305                 310                 315

Leu Arg Ala Gln Leu Arg Met Leu Ala Ser Gln Ala Ser Ala Gly
                320                 325                 330

Arg Arg Leu Ser Asp Val Arg Gly Gly Leu Leu Arg Leu Ala Glu
                335                 340                 345

Ala Leu Ala Phe Arg Gln Asp Leu Glu Val Val Ser Ser Thr Val
                350                 355                 360

Arg Ala Val Ile Ala Thr Leu Arg Ser Gly Glu Gln Cys Ser Val
                365                 370                 375

Glu Pro Asp Leu Ile Ser Lys Val Leu Gln Gly Leu Ile Glu Val
                380                 385                 390

Arg Ser Pro His Leu Glu Glu Leu Leu Thr Ala Phe Phe Ser Ala
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28

Thr Ala Asp Ala Ala Ser Pro Phe Pro Ala Cys Lys Pro Val Val
            410   415   420

Val Val Ser Ser Leu Leu Leu Gln Glu Glu Glu Pro Leu Ala Gly
            425   430   435

Gly Lys Pro Gly Ala Asp Gly Gly Ser Leu Glu Ala Val Arg Leu
            440   445   450

Gly Pro Ser Ser Gly Leu Leu Val Asp Trp Leu Glu Met Leu Asp
            455   460   465

Pro Glu Val Val Ser Ser Cys Pro Asp Leu Gln Leu Arg Leu Leu
            470   475   480

Phe Ser Arg Arg Lys Gly Lys Gly Gln Ala Gln Val Pro Ser Phe
            485   490   495

Arg Pro Tyr Leu Leu Thr Leu Phe Thr His Gln Ser Ser Trp Pro
            500   505   510

Thr Leu His Gln Cys Ile Arg Val Leu Leu Gly Lys Ser Arg Glu
            515   520   525

Gln Arg Phe Asp Pro Ser Ala Ser Leu Asp Phe Leu Trp Ala Cys
            530   535   540

Ile His Val Pro Arg Ile Trp Gln Gly Arg Asp Gln Arg Thr Pro
            545   550   555

Gln Lys Arg Arg Glu Glu Leu Val Leu Arg Val Gln Gly Pro Glu
            560   565   570

Leu Ile Ser Leu Val Glu Leu Ile Leu Ala Glu Ala Glu Thr Arg
            575   580   585

Ser Gln Asp Gly Asp Thr Ala Ala Cys Ser Leu Ile Gln Ala Arg
            590   595   600

Leu Pro Leu Leu Leu Ser Cys Cys Cys Gly Asp Asp Glu Ser Val
            605   610   615

Arg Lys Val Thr Glu His Leu Ser Gly Cys Ile Gln Gln Trp Gly
            620   625   630

Asp Ser Val Leu Gly Arg Arg Cys Arg Asp Leu Leu Leu Gln Leu
            635   640   645

Tyr Leu Gln Arg Pro Glu Leu Arg Val Pro Val Pro Glu Val Leu
            650   655   660

Leu His Ser Glu Gly Ala Ala Ser Ser Ser Val Cys Lys Leu Asp
            665   670   675

Gly Leu Ile His Arg Phe Ile Thr Leu Leu Ala Asp Thr Ser Asp
            680   685   690

29

Ser Arg Ala Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys
            695   700   705

Arg Lys Leu Ala Val Ala His Pro Leu Leu Leu Arg His Leu
            710   715   720

Pro Met Ile Ala Ala Leu Leu His Gly Arg Thr His Leu Asn Phe
            725   730   735

Gln Glu Phe Arg Gln Gln Asn His Leu Ser Cys Phe Leu His Val
            740   745   750

Leu Gly Leu Leu Glu Leu Leu Gln Pro His Val Phe Arg Ser Glu
            755   760   765

His Gln Gly Ala Leu Trp Asp Cys Leu Leu Ser Phe Ile Arg Leu
            770   775   780

Leu Leu Asn Tyr Arg Lys Ser Ser Arg His Leu Ala Ala Phe Ile
            785   790   795

Asn Lys Phe Val Gln Phe Ile His Lys Tyr Ile Thr Tyr Asn Ala
            800   805   810

Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala Asp Pro Leu His
            815   820   825

Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu Lys Ser Leu
            830   835   840

Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr Asp Arg
            845   850   855

Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser Leu
            860   865   870

Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu
            875   880   885

Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu
            890   895   900

Asp Leu Leu Glu Val Leu Ser Asp Ile Asp Glu Met Ser Arg Arg
            905   910   915

Arg Pro Glu Ile Leu Ser Phe Phe Ser Thr Asn Leu Gln Arg Leu
            920   925   930

Met Ser Ser Ala Glu Glu Cys Cys Arg Asn Leu Ala Phe Ser Leu
            935   940   945

Ala Leu Arg Ser Met Gln Asn Ser Pro Ser Ile Ala Ala Ala Phe
            950   955   960

Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln Asp Phe Glu Val
            965   970   975

Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala Leu Leu Cys

                              30

Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly
                    995   1000   1005

Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu
                    1010   1015   1020

Arg Ile Leu His Met Glu Ala Val Met
                    1025

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<211> 2186
<212> DNA
<213> Homo sapiens

<400> 23
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 cgccttcctc tcgctgtcct ggtacgcggc actcagcggc cagaaaggcg 150

 acgttgtgga cgtttaccag cgggagttcc tggcgctgcg cgatcggttg 200

 cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggt 250

 gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgcgagacg 300

 gagacggcaa tcgcacctgg ggccgcctaa cagaggaccc ccgattgaag 350

 ccgtggaacg gctcacaccg gcacgtgctg cacctgccca ccgtcttcca 400

 tcacctgcca cacctgctgg ccaaggagag cagtctgcag cccgcggtgc 450

 gcgtgggcca gggccgcacc ggagtgtcgg tggtgatggg catcccgagc 500

 gtgcggcgcg aggtgcactc gtacctgact gacactctgc actcgctcat 550

 ctccgagctg agcccgcagg agaaggagga ctcggtcatc gtggtgctga 600

 tcgccgagac tgactcacag tacacttcgg cagtgacaga gaacatcaag 650

 gccttgttcc ccacggagat ccattctggg ctcctggagg tcatctcacc 700

 ctccccccac ttctaccctg acttctcccg cctccgagag tcctttgggg 750

 accccaagga gagagtcagg tggaggacca aacagaacct cgattactgc 800

 ttcctcatga tgtacgcgca gtccaaaggc atctactacg tgcagctgga 850

 ggatgacatc gtggccaagc ccaactacct gagcaccatg aagaactttg 900

 cactgcagca gccttcagag gactggatga tcctggagtt ctcccagctg 950

 ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 1000

 gttcattctc atgttctacc gggacaagcc catcgactgg ctcctggacc 1050

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gaccggcaga aagccaacct gcggatccgc ttcaaaccgt ccctcttcca 1150

gcacgtgggc actcactcct cgctggctgg caagatccag aaactgaagg 1200

acaaagactt tggaaagcag gcgctgcgga aggagcatgt gaacccgcca 1250

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attcttggat acatttgatt ttttcacgta agtccacata tacttctata 2100

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<210> 24
<211> 548
<212> PRT
<213> Homo sapiens

<400> 24
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Leu Cys Ala Phe Leu Ser Leu Ser Trp Tyr Ala Ala Leu Ser Gly
              20                  25                  30
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32

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Gln Lys Gly Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala
                35                  40                      45

Leu Arg Asp Arg Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg
                50                  55                      60

Ser Lys Glu Leu Asn Leu Val Leu Asp Glu Ile Lys Arg Ala Val
                65                  70                      75

Ser Glu Arg Gln Ala Leu Arg Asp Gly Asp Gly Asn Arg Thr Trp
                80                  85                      90

Gly Arg Leu Thr Glu Asp Pro Arg Leu Lys Pro Trp Asn Gly Ser
                95                  100                     105

His Arg His Val Leu His Leu Pro Thr Val Phe His His Leu Pro
                110                 115                     120

His Leu Leu Ala Lys Glu Ser Ser Leu Gln Pro Ala Val Arg Val
                125                 130                     135

Gly Gln Gly Arg Thr Gly Val Ser Val Val Met Gly Ile Pro Ser
                140                 145                     150

Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp Thr Leu His Ser
                155                 160                     165

Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp Ser Val Ile
                170                 175                     180

Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser Ala Val
                185                 190                     195

Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser Gly
                200                 205                     210

Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe
                215                 220                     225

Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg
                230                 235                     240

Trp Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr
                245                 250                     255

Ala Gln Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile
                260                 265                     270

Val Ala Lys Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu
                275                 280                     285

Gln Gln Pro Ser Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu
                290                 295                     300

Gly Phe Ile Gly Lys Met Phe Lys Ser Leu Asp Leu Ser Leu Ile
                305                 310                     315

Val Glu Phe Ile Leu Met Phe Tyr Arg Asp Lys Pro Ile Asp Trp
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33

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                    320                 325                 330

    Leu Leu Asp His Ile Leu Trp Val Lys Val Cys Asn Pro Glu Lys
                    335                 340                 345

    Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn Leu Arg Ile Arg
                    350                 355                 360

    Phe Lys Pro Ser Leu Phe Gln His Val Gly Thr His Ser Ser Leu
                    365                 370                 375

    Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys Asp Phe Gly Lys Gln
                    380                 385                 390

    Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala Glu Val Ser Thr
                    395                 400                 405

    Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr Leu
                    410                 415                 420

    Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly Asp Phe
                    425                 430                 435

    Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe Phe
                    440                 445                 450

    Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn
                    455                 460                 465

    Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys
                    470                 475                 480

    Glu Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg
                    485                 490                 495

    Ser Pro Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val
                    500                 505                 510

    Ala Glu Gly Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu
                    515                 520                 525

    Arg Leu Ser Ile Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser
                    530                 535                 540

    Glu Ile Phe Leu Lys Lys Ala Asp
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<210> 25
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 25
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34

<210> 26
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

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<210> 27
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 27
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<210> 28
<211> 23
<212> DNA
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<400> 28
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<210> 29
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 29
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<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 30
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<210> 31
<211> 25
<212> DNA

35

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 31
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<210> 32
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 32
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<210> 33
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<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 33
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<400> 34
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<400> 35
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<210> 36
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<223> Synthetic Oligonucleotide Probe

<400> 36
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<210> 37
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<223> Synthetic Oligonucleotide Probe

<400> 37
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<210> 38
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<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 38
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